

**In the specification**

1. Please Amend Table 2B on page 28 as follows:

**Table 2B Polymerase Domain Mutations in Various DNA Polymerases**

| Enzyme    | Domain (bp) | Domain sequence | Predicted Mutations for Reducing DNA Polymerase Activity# |
|-----------|-------------|-----------------|---|
|           | DXXSLYP     |                 |   |
| Pfu       | 405-411     | DFRALYP         | D405 (D405E)  |
| Tgo       | 404-410     | DFRSLYP         | D404 (D404E)  |
| KOD       | 404-410     | DFRSLYP         | D404 (D404E)  |
| Vent      | 407-413     | DFRSLYP         | D407 [(D404E)] <u>D407E</u>                               |
| Deep Vent | 405-411     | DFRSLYP         | D405 [(D404E)] <u>D405E</u>                               |
|           | YXDTDS      |                 |   |
| Pfu       | 539-544     | YIDTDG          | T542, D543 (T542P; D543G)                                 |
| Tgo       | 538-543     | YADTDG          | T541, D542 (T541P; D542G)                                 |
| KOD       | 538-543     | YSDDTG          | T541, D542 (T541P; D542G)                                 |
| Vent      | 541-546     | YADTDG          | T544, D545 (T544P; D545G)                                 |
| Deep Vent | 539-544     | YIDTDG          | T542, D543 (T542P; D543G)                                 |
|           | KXY         |                 |   |
| Pfu       | 593-595     | KRY             | K593 (K593T)  |
| Tgo       | 592-594     | KKY             | K592 (K592T)  |
| KOD       | 592-594     | KKY             | K592 (K592T)  |
| Vent      | 595-597     | KRY             | K595 (K595T)  |
| Deep      |             |                 |   |

|      |         |     |              |
|------|---------|-----|--------------|
| Vent | 593-595 | KKY | K593 (K593T) |
|------|---------|-----|--------------|

2. On page 19, before the full paragraph starting with “Enzymes possessing 3’-5’ exonuclease activity” and ends with “Preferably, the enzyme comprising 3’-5’ exonuclease activity is a DNA polymerase,” please add the following text:

--Amino acid sequence of JDF-3 DNA polymerase (Sequence 2 of WO 01/32887):

```

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
1           5           10           15
Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
           20           25           30
Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
           35           40           45
Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
           50           55           60
Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
65           70           75           80
Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
           85           90           95
Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
           100          105          110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
           115          120          125
Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
           130          135          140
Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
145          150          155          160

```

|   |     |     |     |
|---|-----|-----|-----|
| Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile |     |     |     |
| 165   | 170 | 175 |     |
| Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys |     |     |     |
| 180   | 185 | 190 |     |
| Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr |     |     |     |
| 195   | 200 | 205 |     |
| Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu |     |     |     |
| 210   | 215 | 220 |     |
| Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys |     |     |     |
| 225   | 230 | 235 | 240 |
| Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val |     |     |     |
| 245   | 250 | 255 |     |
| His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr |     |     |     |
| 260   | 265 | 270 |     |
| Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu |     |     |     |
| 275   | 280 | 285 |     |
| Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly |     |     |     |
| 290   | 295 | 300 |     |
| Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr |     |     |     |
| 305   | 310 | 315 | 320 |
| Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu |     |     |     |
| 325   | 330 | 335 |     |
| Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu |     |     |     |
| 340   | 345 | 350 |     |
| Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala |     |     |     |
| 355   | 360 | 365 |     |

Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr  
370 375 380  
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile  
385 390 395 400  
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His  
405 410 415  
Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp  
420 425 430  
Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe  
435 440 445  
Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys  
450 455 460  
Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp  
465 470 475 480  
Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr  
485 490 495  
Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser  
500 505 510  
Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu  
515 520 525  
Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu  
530 535 540  
His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala  
545 550 555 560  
Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu  
565 570 575  
Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys

|   |     |     |     |
|---|-----|-----|-----|
| 580   | 585 | 590 |     |
| Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu |     |     |     |
| 595   | 600 | 605 |     |
| Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala |     |     |     |
| 610   | 615 | 620 |     |
| Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val |     |     |     |
| 625   | 630 | 635 | 640 |
| Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro |     |     |     |
| 645   | 650 | 655 |     |
| Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp |     |     |     |
| 660   | 665 | 670 |     |
| Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala |     |     |     |
| 675   | 680 | 685 |     |
| Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu |     |     |     |
| 690   | 695 | 700 |     |
| Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe |     |     |     |
| 705   | 710 | 715 | 720 |
| Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln |     |     |     |
| 725   | 730 | 735 |     |
| Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys |     |     |     |
| 740   | 745 | 750 |     |
| Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp |     |     |     |
| 755   | 760 | 765 |     |
| Leu Lys Pro Lys Gly Lys Lys Lys (SEQ ID NO: 10)                 |     |     |     |
| 770   | 775 |     |     |

## --Nucleotide sequence of JDF-3 DNA polymerase (Sequence 1 of WO 01/32887)

```

atgatccttg acgttgatta catcaccgag aatggaaagc ccgtcatcag ggtcttcaag      60
aaggagaacg gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg      120
ctcctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc      180
agggtcgtta aggttaagcg cgcggagaag gtgaagaaaa agttcctcgg caggtctgtg      240
gaggtctggg tcctctactt cacgcacccg caggacgttc cggcaatccg cgacaaaata      300
aggaagcacc ccgcggtcac cgacatctac gagtacgaca tacccttcgc caagcgctac      360
ctcatagaca agggcctaac cccgatggaa ggtgaggaag agcttaaact catgtccttc      420
gacatcgaga cgctctacca cgagggagaa gagtttgaa ccgggccgat tctgatgata      480
agctacgccg atgaaagcga ggcgcgcgtg ataacctgga agaagatcga ccttccttac      540
gttgaggttg tctccaccga gaaggagatg attaagcgct tcttgagggg cgttaaggag      600
aaggacccgg acgtgctgat aacatacaac ggcgacaact tcgacttcgc ctacctgaaa      660
aagcgctgtg agaagcttgg cgtgagcttt accctcgga gggacgggag cgagccgaag      720
atacagcgca tgggggacag gtttgcggtc gaggtgaagg gcagggtaca cttcgacctt      780
tatccagtca taaggcgcac cataaacctc ccgacctaca cccttgaggc tgtatacgag      840
gcggttttcg gcaagcccaa ggagaaggtc tacgccgagg agatagccac cgcctgggag      900
accggcgagg ggcttgagag ggtcgcgcgc tactcgatgg aggacgcgag ggttacctac      960
gagcttgga gggagttctt cccgatggag gccagcttt ccaggctcat cggccaaggc      1020
ctctgggacg tttcccgcgc cagcaccggc aacctcgctg agtggttcct cctaaggaag      1080
gcctacgaga ggaacgaact cgctcccaac aagcccgcg agagggagct ggcgaggaga      1140
agggggggct acgccggtgg ctacgtcaag gagccggagc ggggactgtg ggacaatatc      1200
gtgtatctag actttcgtag tctctaccct tcaatcataa tcaccacaa cgtctcgcca      1260
gatacgctca accgcgaggg gtgtaggagc tacgacgttg ccccgagggt cggtcacaag      1320
ttctgcaagg acttccccgg cttcattccg agcctgctcg gaaacctgct ggaggaaagg      1380
cagaagataa agaggaagat gaaggcaact ctcgaccgcg tggagaagaa tctcctcgat      1440
tacaggcaac gcgccatcaa gattctcgcc aacagctact acggctacta cggctatgcc      1500
agggcaagat ggtactgcag ggagtgcgcc gagagcggtta cggcatgggg aaggaggtag      1560

```

```
atcgaaatgg tcatcagaga gcttgaggaa aagttcggtt ttaaagtcct ctatgcagac 1620
acagacggtc tccatgccac cattcctgga gcggacgctg aaacagtcaa gaaaaaggca 1680
atggagttct taaactatat caatcccaaa ctgcccggcc ttctcgaact cgaatacgag 1740
ggcttctacg tcaggggctt cttcgtcacg aagaaaaagt acgcggtcat cgacgaggag 1800
ggcaagataa ccacgcgcgg gcttgagata gtcaggcgcg actggagcga gatagcgaag 1860
gagacgcagg cgaggggtttt ggaggcgata ctcaggcacg gtgacgttga agaggccgtc 1920
agaattgtca gggaagtcac cgaaaagctg agcaagtacg aggttccgcc ggagaagctg 1980
gttatccacg agcagataac gcgcgagctc aaggactaca aggccaccgg cccgcacgta 2040
gccatagcga agcgtttggc cgccagaggt gttaaaatcc ggcccggaac tgtgataagc 2100
tacatcgttc tgaagggtc cggaaggata ggcgacaggc cgattccctt cgacgagttc 2160
gacccgacga agcacaagta cgatgcggac tactacatcg agaaccaggt tctgccggca 2220
gttgagagaa tcctcagggc cttcggtac cgcaaggaag acctgcgcta ccagaagacg 2280
aggcaggtcg ggcttggcgc gtggctgaag ccgaagggga agaagaagtg a 2331 (SEQ ID NO: 11)
```